

1633

RAW SEQUENCE LISTING

DATE: 07/05/2001

PATENT APPLICATION: US/09/327,750C

TIME: 12:58:15

Input Set : A:\ES.txt

Output Set: N:\CRF3\07032001\I327750C.raw

3 <110> APPLICANT: Sato, Taki-Aki
 5 <120> TITLE OF INVENTION: GENE ENCODING NADE, P75NTR- ASSOCIATED CELL DEATH EXECUTOR
 AND USES
 6 THEREOF
 8 <130> FILE REFERENCE: 0575/59131/JPW/APE
 10 <140> CURRENT APPLICATION NUMBER: 09/327,750C
 11 <141> CURRENT FILING DATE: 1999-06-07
 13 <160> NUMBER OF SEQ ID NOS: 45
 15 <170> SOFTWARE: PatentIn version 3.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 36
 19 <212> TYPE: DNA
 20 <213> ORGANISM: MOUSE
 22 <400> SEQUENCE: 1
 23 aattgtctac gcatccttat gggggagctg tctaac 36
 26 <210> SEQ ID NO: 2
 27 <211> LENGTH: 12
 28 <212> TYPE: PRT
 29 <213> ORGANISM: MOUSE
 31 <400> SEQUENCE: 2
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 34 1 5 10
 36 <210> SEQ ID NO: 3
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 38 <212> TYPE: DNA
 39 <213> ORGANISM: Artificial Sequence
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 42 <221> NAME/KEY: misc_feature
 43 <222> LOCATION: (1)..(30)
 44 <223> OTHER INFORMATION: Mouse Nade DNA
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 48 ctagctagca tcatggtgag caagggcgag 30
 51 <210> SEQ ID NO: 4
 52 <211> LENGTH: 28
 53 <212> TYPE: DNA
 54 <213> ORGANISM: Artificial Sequence
 56 <220> FEATURE:
 57 <221> NAME/KEY: misc_feature
 58 <222> LOCATION: (1)..(28)
 59 <223> OTHER INFORMATION: Mouse Nade DNA
 62 <400> SEQUENCE: 4
 63 ccgctcgagt cttgtacagc tcgtccat 28
 66 <210> SEQ ID NO: 5
 67 <211> LENGTH: 29
 68 <212> TYPE: DNA
 69 <213> ORGANISM: Artificial Sequence
 71 <220> FEATURE:
 72 <221> NAME/KEY: misc_feature

Does Not Comply
 Corrected Diskette Needed

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73 <222> LOCATION: (1)..(29)
74 <223> OTHER INFORMATION: Mouse Nade DNA
77 <400> SEQUENCE: 5
78 atcctcgagc gatcatggcc aatgtccac 29
81 <210> SEQ ID NO: 6
82 <211> LENGTH: 27
83 <212> TYPE: DNA
C--> 84 <213> ORGANISM: Artificial Sequence
86 <220> FEATURE:
87 <221> NAME/KEY: misc_feature
88 <222> LOCATION: ()..()
89 <223> OTHER INFORMATION: Mouse Nade DNA
92 <400> SEQUENCE: 6
93 atcggatcct ctcagctgta gctccct 27
96 <210> SEQ ID NO: 7
97 <211> LENGTH: 27
98 <212> TYPE: DNA
99 <213> ORGANISM: Artificial Sequence
101 <220> FEATURE:
102 <221> NAME/KEY: misc_feature
103 <222> LOCATION: (1)..(27)
104 <223> OTHER INFORMATION: Mouse Nade DNA
107 <400> SEQUENCE: 7
108 atcggatccg atctctctca tctctc 27
111 <210> SEQ ID NO: 8
112 <211> LENGTH: 27
113 <212> TYPE: DNA
114 <213> ORGANISM: Artificial Sequence
116 <220> FEATURE:
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118 <222> LOCATION: (1)..(27)
119 <223> OTHER INFORMATION: Mouse Nade DNA
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123 aaagcttagg gaggcacagc tgagaaa 27
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129 <213> ORGANISM: Artificial Sequence
131 <220> FEATURE:
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133 <222> LOCATION: (1)..(27)
134 <223> OTHER INFORMATION: Mouse Nade DNA
137 <400> SEQUENCE: 9
138 tttctcagct gtgcctccct aagcttt 27
141 <210> SEQ ID NO: 10
142 <211> LENGTH: 26
143 <212> TYPE: DNA
144 <213> ORGANISM: Artificial Sequence
146 <220> FEATURE:

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TIME: 12:58:15

Input Set : A:\ES.txt

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163 <222> LOCATION: (1)..(26)
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174 <213> ORGANISM: MOUSE
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179 1 5 10 15
181 Asn Gly Glu Glu Asp Arg Pro Val Gly Gly Gly Glu Gly His Gln Pro
182 20 25 30
184 Ala Gly Asn Asn Asn Asn Asn Asn His Asn His Asn His Asn His His
185 35 40 45
187 Arg Arg Gly Gln Ala Arg Arg Leu Ala Pro Asn Phe Arg Trp Ala Ile
188 50 55 60
190 Pro Asn Arg Gln Met Asn Asp Gly Leu Gly Gly Asp Gly Asp Asp Met
191 65 70 75 80
193 Glu Met Phe Met Glu Glu Met Arg Glu Ile Arg Arg Lys Leu Arg Glu
194 85 90 95
196 Leu Gln Leu Arg Asn Cys Leu Arg Ile Leu Met Gly Glu Leu Ser Asn
197 100 105 110
199 His His Asp His His Asp Glu Phe Cys Leu Met Pro
200 115 120
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204 <212> TYPE: PRT
205 <213> ORGANISM: HUMAN
207 <400> SEQUENCE: 13
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212 Asn Gly Glu Glu Asp Arg Pro Leu Gly Gly Gly Glu Gly His Gln Pro
213 20 25 30
215 Ala Gly Asn Arg Arg Gly Gln Ala Arg Arg Leu Ala Pro Asn Phe Arg
216 35 40 45
218 Trp Ala Ile Pro Asn Arg Gln Ile Asn Asp Gly Met Gly Gly Asp Gly
219 50 55 60

```

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TIME: 12:58:15

Input Set : A:\ES.txt

Output Set: N:\CRF3\07032001\I327750C.raw

221 Asp Asp Met Glu Ile Phe Met Glu Glu Met Arg Glu Ile Arg Arg Lys
 222 65 70 75 80
 224 Leu Arg Glu Leu Gln Leu Arg Asn Cys Leu Arg Ile Leu Met Gly Glu
 225 85 90 95
 227 Leu Ser Asn His His Asp His His Asp Glu Phe Cys Leu Met Pro
 228 100 105 110
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 231 <211> LENGTH: 13
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 238 1 5 10
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 243 <213> ORGANISM: MAPKK
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 258 1 5 10
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 263 <213> ORGANISM: TF III A
 265 <400> SEQUENCE: 17
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 268 1 5
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 273 <213> ORGANISM: Rev HIV-1
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 280 <210> SEQ ID NO: 19
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 282 <212> TYPE: PRT
 283 <213> ORGANISM: Ran_BP1
 285 <400> SEQUENCE: 19
 287 Lys Val Ala Glu Lys Leu Glu Ala Leu Ser Val Arg
 288 1 5 10
 290 <210> SEQ ID NO: 20

sec item # 10 on
 ERROR SUMMARY SHEET

RAW SEQUENCE LISTING

DATE: 07/05/2001

PATENT APPLICATION: US/09/327,750C

TIME: 12:58:15

Input Set : A:\ES.txt

Output Set: N:\CRF3\07032001\I327750C.raw

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292 <212> TYPE: PRT
293 <213> ORGANISM: FMRP
295 <400> SEQUENCE: 20
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300 <210> SEQ ID NO: 21
301 <211> LENGTH: 8
302 <212> TYPE: PRT
303 <213> ORGANISM: Gle 1 — see page 4
305 <400> SEQUENCE: 21
307 Leu Pro Leu Gly Lys Leu Thr Leu
308 1 5
310 <210> SEQ ID NO: 22
311 <211> LENGTH: 14
312 <212> TYPE: PRT
313 <213> ORGANISM: Rex HTLV-1
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317 Ala Leu Ser Ala Gln Leu Tyr Ser Ser Leu Ser Leu Asp Ser
318 1 5 10
320 <210> SEQ ID NO: 23
321 <211> LENGTH: 13
322 <212> TYPE: PRT
323 <213> ORGANISM: human NADE
325 <400> SEQUENCE: 23
327 Arg Glu Ile Arg Arg Lys Leu Arg Glu Leu Gln Leu Arg
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333 <213> ORGANISM: mouse NADE
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343 <213> ORGANISM: MOUSE
345 <400> SEQUENCE: 25
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351 20 25
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355 <212> TYPE: PRT
356 <213> ORGANISM: HUMAN
358 <400> SEQUENCE: 26
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VERIFICATION SUMMARY

DATE: 07/05/2001

PATENT APPLICATION: US/09/327,750C

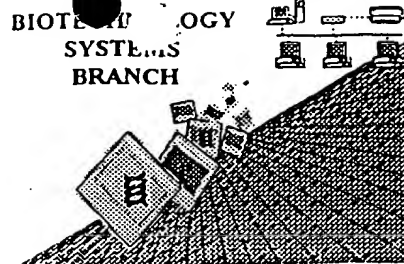
TIME: 12:58:16

Input Set : A:\ES.txt

Output Set: N:\CRF3\07032001\I327750C.raw

L:84 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6

RAW SEQUENCE LISTING ERROR REPORT



15
OCT 18 2001
TECH CENTER 1600/2900

RECEIVED

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/327,750C

Source: 1633

Date Processed by STIC: 7/5/2001

RECEIVED

JUL 23 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other:

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support (SIRA)

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/327,750 C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text**.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

- 10 ✓ Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.